



1600

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MAY 27 2003

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/848,909A

DATE: 05/20/2003

TIME: 17:26:37

Input Set : A:\00742.060002.SEQLIST.TXT

Output Set: N:\CRF4\05202003\I848909A.raw

4 <110> APPLICANT: Collier, R. John
 5 Sellman, Brett R.
 7 <120> TITLE OF INVENTION: Compounds and Methods for the Treatment
 8 and Prevention of Bacterial Infection
 11 <130> FILE REFERENCE: 00742/060002
 13 <140> CURRENT APPLICATION NUMBER: US 09/848,909A
 14 <141> CURRENT FILING DATE: 2001-05-04
 16 <150> PRIOR APPLICATION NUMBER: US 60/201,800
 17 <151> PRIOR FILING DATE: 2000-05-04
 19 <160> NUMBER OF SEQ ID NOS: 35
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 735
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Bacillus anthracis
 28 <400> SEQUENCE: 1
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 31 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
 32 20 25 30
 33 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
 34 35 40 45
 35 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
 36 50 55 60
 37 Trp Ser Gly Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala
 38 65 70 75 80
 39 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
 40 85 90 95
 41 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
 42 100 105 110
 43 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
 44 115 120 125
 45 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
 46 130 135 140
 47 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
 48 145 150 155 160
 49 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
 50 165 170 175
 51 Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr
 52 180 185 190
 53 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
 54 195 200 205
 55 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu

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56      210      215      220
57 Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr
58 225      230      235      240
59 Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val
60      245      250      255
61 Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser
62      260      265      270
63 Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr
64      275      280      285
65 Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His
66      290      295      300
67 Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val
68 305      310      315      320
69 Ser Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His
70      325      330      335
71 Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu
72      340      345      350
73 Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn
74      355      360      365
75 Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val
76      370      375      380
77 Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Ala Glu Asn Gln
78 385      390      395      400
79 Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu
80      405      410      415
81 Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile
82      420      425      430
83 Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu
84      435      440      445
85 Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe
86      450      455      460
87 Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val
88 465      470      475      480
89 Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys
90      485      490      495
91 Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp
92      500      505      510
93 Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys
94      515      520      525
95 Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly
96      530      535      540
97 Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln
98 545      550      555      560
99 Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr
100      565      570      575
101 Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg
102      580      585      590
103 Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp
104      595      600      605

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105 Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr
106      610      615      620
107 Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser
108 625      630      635      640
109 Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile
110      645      650      655
111 Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly
112      660      665      670
113 Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr
114      675      680      685
115 Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu
116      690      695      700
117 Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly
118 705      710      715      720
119 Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
120      725      730      735
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 735
125 <212> TYPE: PRT
126 <213> ORGANISM: Bacillus anthracis
128 <400> SEQUENCE: 2
129 Glu Val Lys Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser
130 1      5      10      15
131 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
132      20      25      30
133 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
134      35      40      45
135 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
136      50      55      60
137 Trp Ser Gly Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala
138 65      70      75      80
139 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
140      85      90      95
141 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
142      100      105      110
143 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
144      115      120      125
145 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
146      130      135      140
147 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
148 145      150      155      160
149 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
150      165      170      175
151 Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr
152      180      185      190
153 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
154      195      200      205
155 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu
156      210      215      220

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157 Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr
158 225 230 235 240
159 Gly Arg Ile Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val
160 245 250 255
161 Ala Ala Tyr Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser
162 260 265 270
163 Lys Asn Glu Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr
164 275 280 285
165 Ile Ser Lys Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His
166 290 295 300
167 Gly Asn Ala Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val
168 305 310 315 320
169 Ser Ala Gly Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His
170 325 330 335
171 Ser Leu Ser Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu
172 340 345 350
173 Asn Thr Ala Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn
174 355 360 365
175 Thr Gly Thr Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val
176 370 375 380
177 Leu Gly Lys Asn Gln Thr Leu Ala Thr Ile Lys Ala Asp Glu Asn Gln
178 385 390 395 400
179 Leu Ser Gln Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu
180 405 410 415
181 Ala Pro Ile Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile
182 420 425 430
183 Thr Met Asn Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu
184 435 440 445
185 Arg Leu Asp Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe
186 450 455 460
187 Glu Asn Gly Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val
188 465 470 475 480
189 Leu Pro Gln Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys
190 485 490 495
191 Asp Leu Asn Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp
192 500 505 510
193 Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys
194 515 520 525
195 Ile Ala Phe Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly
196 530 535 540
197 Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln
198 545 550 555 560
199 Asn Ile Lys Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr
200 565 570 575
201 Val Leu Asp Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg
202 580 585 590
203 Asp Lys Arg Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp
204 595 600 605
205 Glu Ser Val Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr

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```

206      610      615      620
207 Glu Gly Leu Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser
208 625      630      635      640
209 Gly Tyr Ile Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile
210      645      650      655
211 Asn Asp Arg Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly
212      660      665      670
213 Lys Thr Phe Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr
214      675      680      685
215 Ile Ser Asn Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu
216      690      695      700
217 Asn Thr Ile Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly
218 705      710      715      720
219 Ile Lys Lys Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
220      725      730      735
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 735
225 <212> TYPE: PRT
226 <213> ORGANISM: Bacillus anthracis
228 <400> SEQUENCE: 3
229 Glu Val Lys Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser
230 1      5      10      15
231 Gln Gly Leu Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro
232      20      25      30
233 Met Val Val Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser
234      35      40      45
235 Glu Leu Glu Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile
236      50      55      60
237 Trp Ser Gly Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala
238 65      70      75      80
239 Thr Ser Ala Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val
240      85      90      95
241 Ile Asn Lys Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg
242      100      105      110
243 Leu Tyr Gln Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys
244      115      120      125
245 Gly Leu Asp Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu
246      130      135      140
247 Val Ile Ser Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser
248 145      150      155      160
249 Ser Asn Ser Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro
250      165      170      175
251 Asp Arg Asp Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr
252      180      185      190
253 Thr Val Asp Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser
254      195      200      205
255 Asn Ile His Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu
256      210      215      220
257 Lys Trp Ser Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/20/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 397

Seq#:23; Xaa Pos. 427